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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/081,301

DATE: 03/07/2002

TIME: 11:23:36

Input Set : N:\Crf3\RULE60\10081301.txt
Output Set: N:\CRF3\03072002\J081301.raw

3 <110> APPLICANT: Falco, S. Carl
4 Cahoon, Rebecca E.
5 Rafalski, J. Antoni
7 <120> TITLE OF INVENTION: Vitamin B Metabolism Proteins
9 <130> FILE REFERENCE: BB-1201
11 <140> CURRENT APPLICATION NUMBER: 10/081,301
12 <141> CURRENT FILING DATE: 2002-02-20
14 <150> PRIOR APPLICATION NUMBER: 09/371,056
15 <151> PRIOR FILING DATE: 1999-08-09
17 <150> PRIOR APPLICATION NUMBER: 60/096,342
W--> 18 <151> PRIOR FILING DATE: August 12, 1998
20 <160> NUMBER OF SEQ ID NOS: 16
22 <170> SOFTWARE: Microsoft Office 97
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 933
26 <212> TYPE: DNA
27 <213> ORGANISM: Zea mays
29 <400> SEQUENCE: 1
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31 atccagtccc acaccgtcca ggggtatgtt ggcaacaaat cggccgtctt tcccctgcag 120
32 ctccttggct ttgatgtgga tccaataaac tctgtacagt tttctaatac tacaggatac 180
33 ccaacattta gaggtcaggt tcttaatggc aaacagctct gggaccttat tgaaggactg 240
34 gagaaaaatc agttgcttca ttatacccat ttattaacag gttatataagg ctcagtttcc 300
35 ttttagata ctgtgtaca agttgtttag aaattgcgtat cagttaatcc tgatcttgta 360
36 tatgtttgtg acccagtctt aggtgtatgaa ggaaaactat atgttcctca ggaggttaata 420
37 tctgtttatc aacagaaggt tttccagtt gcttcaatgc ttacacctaa ccaatttgaa 480
38 gttgaactac ttactggatt gaggtcacc tccgaagaag atgggtttagc agcttgtaat 540
39 accctccaca gtgccggacc acagaagggt gttataacta gtgtcttat tgaaggttaag 600
40 ctgctcccta tcggaagtca caaaaaaaca gaggaacaac agccagaaca atttaagatt 660
41 gagataccaa agataacctgc atatttcacg ggaactggag atttgacaaac tgctctcccta 720
42 ctaggatgga gtaataaaata tcctgtatgc ctcgagaaag cagcagaact ggcagtttcc 780
43 agttgcagg cacttctgaa aagaactgtg gaagactata aaatggccgg cttcgacc 840
44 tcgaccagca gcttagagat ccgggttgatc caaagccagg acgagatccg aaacccaact 900
45 gttacatgca aggctgtgaa gtatggaagc tga 933
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48 <211> LENGTH: 310
49 <212> TYPE: PRT
50 <213> ORGANISM: Zea mays
52 <400> SEQUENCE: 2
53 Met Ala Arg Pro Pro Ile Leu Ser Val Ala Leu Pro Ser Asp Thr Gly
54 1 5 10 15
55 Arg Val Leu Ser Ile Gln Ser His Thr Val Gln Gly Tyr Val Gly Asn
57 20 25 30

ENTERED

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Input Set : N:\Crf3\RULE60\10081301.txt
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59 Lys Ser Ala Val Phe Pro Leu Gln Leu Leu Gly Phe Asp Val Asp Pro
 60 35 40 45
 62 Ile Asn Ser Val Gln Phe Ser Asn His Thr Gly Tyr Pro Thr Phe Arg
 63 50 55 60
 65 Gly Gln Val Leu Asn Gly Lys Gln Leu Trp Asp Leu Ile Glu Gly Leu
 66 65 70 75 80
 68 Glu Glu Asn Gln Leu Leu His Tyr Thr His Leu Leu Thr Gly Tyr Ile
 69 85 90 95
 71 Gly Ser Val Ser Phe Leu Asp Thr Val Leu Gln Val Val Glu Lys Leu
 72 100 105 110
 74 Arg Ser Val Asn Pro Asp Leu Val Tyr Val Cys Asp Pro Val Leu Gly
 75 115 120 125
 77 Asp Glu Gly Lys Leu Tyr Val Pro Gln Glu Val Ile Ser Val Tyr Gln
 78 130 135 140
 80 Gln Lys Val Val Pro Val Ala Ser Met Leu Thr Pro Asn Gln Phe Glu
 81 145 150 155 160
 83 Val Glu Leu Leu Thr Gly Leu Arg Ile Thr Ser Glu Glu Asp Gly Leu
 84 165 170 175
 86 Thr Ala Cys Asn Thr Leu His Ser Ala Gly Pro Gln Lys Val Val Ile
 87 180 185 190
 89 Thr Ser Ala Leu Ile Glu Gly Lys Leu Leu Leu Ile Gly Ser His Lys
 90 195 200 205
 92 Lys Thr Glu Glu Gln Gln Pro Glu Gln Phe Lys Ile Glu Ile Pro Lys
 93 210 215 220
 95 Ile Pro Ala Tyr Phe Thr Gly Thr Gly Asp Leu Thr Thr Ala Leu Leu
 96 225 230 235 240
 98 Leu Gly Trp Ser Asn Lys Tyr Pro Asp Ser Leu Glu Lys Ala Ala Glu
 99 245 250 255
 101 Leu Ala Val Ser Ser Leu Gln Ala Leu Leu Lys Arg Thr Val Glu Asp
 102 260 265 270
 104 Tyr Lys Met Ala Gly Phe Asp Pro Ser Thr Ser Ser Leu Glu Ile Arg
 105 275 280 285
 107 Leu Ile Gln Ser Gln Asp Glu Ile Arg Asn Pro Thr Val Thr Cys Lys
 108 290 295 300
 110 Ala Val Lys Tyr Gly Ser
 111 305 310
 113 <210> SEQ ID NO: 3
 114 <211> LENGTH: 413
 115 <212> TYPE: DNA
 116 <213> ORGANISM: Oryza sativa
 118 <220> FEATURE:
 119 <221> NAME/KEY: unsure
 120 <222> LOCATION: (380)
 122 <220> FEATURE:
 123 <221> NAME/KEY: unsure
 124 <222> LOCATION: (384)
 126 <220> FEATURE:
 127 <221> NAME/KEY: unsure
 128 <222> LOCATION: (388)

RAW SEQUENCE LISTING
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Input Set : N:\Crf3\RULE60\10081301.txt
Output Set: N:\CRF3\03072002\J081301.raw

130 <220> FEATURE:
 131 <221> NAME/KEY: unsure
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 136 ggtggtaata actagtgcac ttattgaaga taagctgctc ctcattggaa gccacaaaaa 120
 137 agcaaaggaa caaccaccag aacaattaa gattgagata cccaaagatac ctgcataattt 180
 138 cacgggact ggagattaa caactgcct tctacttaga tggagtaata aataccctga 240
 139 taaccttgg aagggcgctg aactggcggt atccatttgc aaggcacccc taaggagaac 300
 140 tgtggaaagac tataaaagac tgggtttgac cctccaacca acacctagag atccgcctgg 360
 W--> 141 attcaaaacc aaggatgaan tccnaagncc caagatacat gcaagctgtn aaa 413
 143 <210> SEQ ID NO: 4
 144 <211> LENGTH: 136
 145 <212> TYPE: PRT
 146 <213> ORGANISM: Oryza sativa
 148 <220> FEATURE:
 149 <221> NAME/KEY: UNSURE
 150 <222> LOCATION: (127)..(128)..(129)
 152 <400> SEQUENCE: 4
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 154 1 5 10 15
 156 Gly Pro Arg Lys Val Val Ile Thr Ser Ala Leu Ile Glu Asp Lys Leu
 157 20 25 30
 159 Leu Leu Ile Gly Ser His Lys Lys Ala Lys Glu Gln Pro Pro Glu Gln
 160 35 40 45
 162 Phe Lys Ile Glu Ile Pro Lys Ile Pro Ala Tyr Phe Thr Gly Thr Gly
 163 50 55 60
 165 Asp Leu Thr Thr Ala Leu Leu Gly Trp Ser Asn Lys Tyr Pro Asp
 166 65 70 75 80
 168 Asn Leu Gly Glu Gly Ala Glu Leu Ala Val Ser Ile Cys Lys Ala Pro
 169 85 90 95
 171 Leu Arg Arg Thr Val Glu Asp Tyr Lys Arg Leu Gly Leu Thr Leu Gln
 172 100 105 110
 W--> 174 Pro Thr Pro Arg Asp Pro Pro Gly Phe Lys Thr Lys Asp Glu Xaa Xaa
 175 115 120 125
 W--> 177 Xaa Pro Lys Ile His Ala Ser Cys
 178 130 135
 180 <210> SEQ ID NO: 5
 181 <211> LENGTH: 812
 182 <212> TYPE: DNA
 183 <213> ORGANISM: Glycine max
 185 <220> FEATURE:
 186 <221> NAME/KEY: unsure
 187 <222> LOCATION: (577)
 189 <220> FEATURE:
 190 <221> NAME/KEY: unsure
 191 <222> LOCATION: (610)
 193 <220> FEATURE:
 194 <221> NAME/KEY: unsure

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Input Set : N:\Crf3\RULE60\10081301.txt
Output Set: N:\CRF3\03072002\J081301.raw

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195 <222> LOCATION: (683)
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227 <222> LOCATION: (778)
229 <220> FEATURE:
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233 <220> FEATURE:
234 <221> NAME/KEY: unsure
235 <222> LOCATION: (792)
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239 <222> LOCATION: (804)
241 <400> SEQUENCE: 5
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243 tctcgctcgc tcttccctcg aacaccggtc gagttctcag cattcaatct cacaccgttc 120
244 aggggtatgt tggtaataaaa tccgctgtct tccctctgca actactggga tatgtatgtcg 180
245 atccaattaa ttccgtgcag ttttgcataatc atacaggata tccgacgttt aagggtcagg 240
246 ttttgaatgg acagcaactc tgggatctaa tcgaaggcct tgaaggaaat gatttattgt 300
247 tctatactca cttgctaaca gtttatattg gttcagatc ttttcttaaac actgtattgc 360
248 aagtgtcag caaacttcgg tcaacaaacc caggtcttgc gtatgtatgt gatccagtga 420
249 tgggtgtatga agggaaagctt tatgttccctc aagagcttagt atcagtctat cgtgagaagg 480
250 ttgttccagt agcttcaatg ttgactccca accagttga agcagaacta ctgacaggct 540
W--> 251 ttaggattca gtctgaagga catggccggg aggctgnatg gcttctccat gcagctgggc 600
W--> 252 cttcaaaggn cataattaca agtataaaata tagacggat tcttctcctc attggcagtc 660
W--> 253 atccaaaaga aaagggagag ccncccngac aatttaagat tgttattcca aaaataacca 720
W--> 254 gcttatttta cgggaacggg anancncatg actgnattcn tcttggttng agcataanta 780
W--> 255 cccannacaa ancttgagaa tgcngcggaa ct 812

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Input Set : N:\Crf3\RULE60\10081301.txt
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257 <210> SEQ ID NO: 6
 258 <211> LENGTH: 196
 259 <212> TYPE: PRT
 260 <213> ORGANISM: Glycine max
 262 <220> FEATURE:
 263 <221> NAME/KEY: UNSURE
 264 <222> LOCATION: (178)
 266 <220> FEATURE:
 267 <221> NAME/KEY: UNSURE
 268 <222> LOCATION: (189)
 270 <400> SEQUENCE: 6
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 272 1 5 10 15
 274 Val Leu Ser Ile Gln Ser His Thr Val Gln Gly Tyr Val Gly Asn Lys
 275 20 25 30
 277 Ser Ala Val Phe Pro Leu Gln Leu Leu Gly Tyr Asp Val Asp Pro Ile
 278 35 40 45
 280 Asn Ser Val Gln Phe Ser Asn His Thr Gly Tyr Pro Thr Phe Lys Gly
 281 50 55 60
 283 Gln Val Leu Asn Gly Gln Gln Leu Trp Asp Leu Ile Glu Gly Leu Glu
 284 65 70 75 80
 286 Gly Asn Asp Leu Leu Phe Tyr Thr His Leu Leu Thr Gly Tyr Ile Gly
 287 85 90 95
 289 Ser Glu Ser Phe Leu Asn Thr Val Leu Gln Val Val Ser Lys Leu Arg
 290 100 105 110
 292 Ser Thr Asn Pro Gly Leu Ser Tyr Val Cys Asp Pro Val Met Gly Asp
 293 115 120 125
 295 Glu Gly Lys Leu Tyr Val Pro Gln Glu Leu Val Ser Val Tyr Arg Glu
 296 130 135 140
 298 Lys Val Val Pro Val Ala Ser Met Leu Thr Pro Asn Gln Phe Glu Ala
 299 145 150 155 160
 301 Glu Leu Leu Thr Gly Phe Arg Ile Gln Ser Glu Gly His Gly Arg Glu
 302 165 170 175
 W--> 304 Ala Xaa Arg Leu Leu His Ala Ala Gly Pro Ser Lys Xaa Ile Ile Thr
 305 180 185 190
 307 Ser Ile Asn Ile
 308 195
 310 <210> SEQ ID NO: 7
 311 <211> LENGTH: 773
 312 <212> TYPE: DNA
 313 <213> ORGANISM: Triticum aestivum
 315 <400> SEQUENCE: 7
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 317 atccagtccc acaccgtcca ggggtatgtt ggcaacaaat cggccgtctt tcccctgcag 120
 318 ctccttggtt ttgatgtgga tccaataaac tctgtacagt tttctaatac tacaggatac 180
 319 ccaacattta gagggtcagt tcttaatggc aaacagctct gggacttat tgaaggactg 240
 320 gagggaaaatc agctgcttca ttatacccat ttattaacag gtttatataagg ctcagttcc 300
 321 ttttttagata ctgtgctaca agttgttgag aaattgcgt cagttaatcc tgatcttgc 360
 322 tatgtttgtg acccagttct aggtgatgaa ggaaaactat atgttcctca ggagctaata 420

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10081301.txt
Output Set: N:\CRF3\03072002\J081301.raw

L:18 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:141 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:174 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:177 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:251 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:252 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:253 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:254 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:255 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:304 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:395 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:422 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:570 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:571 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:572 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:573 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:574 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:575 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:576 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:604 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:607 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12